

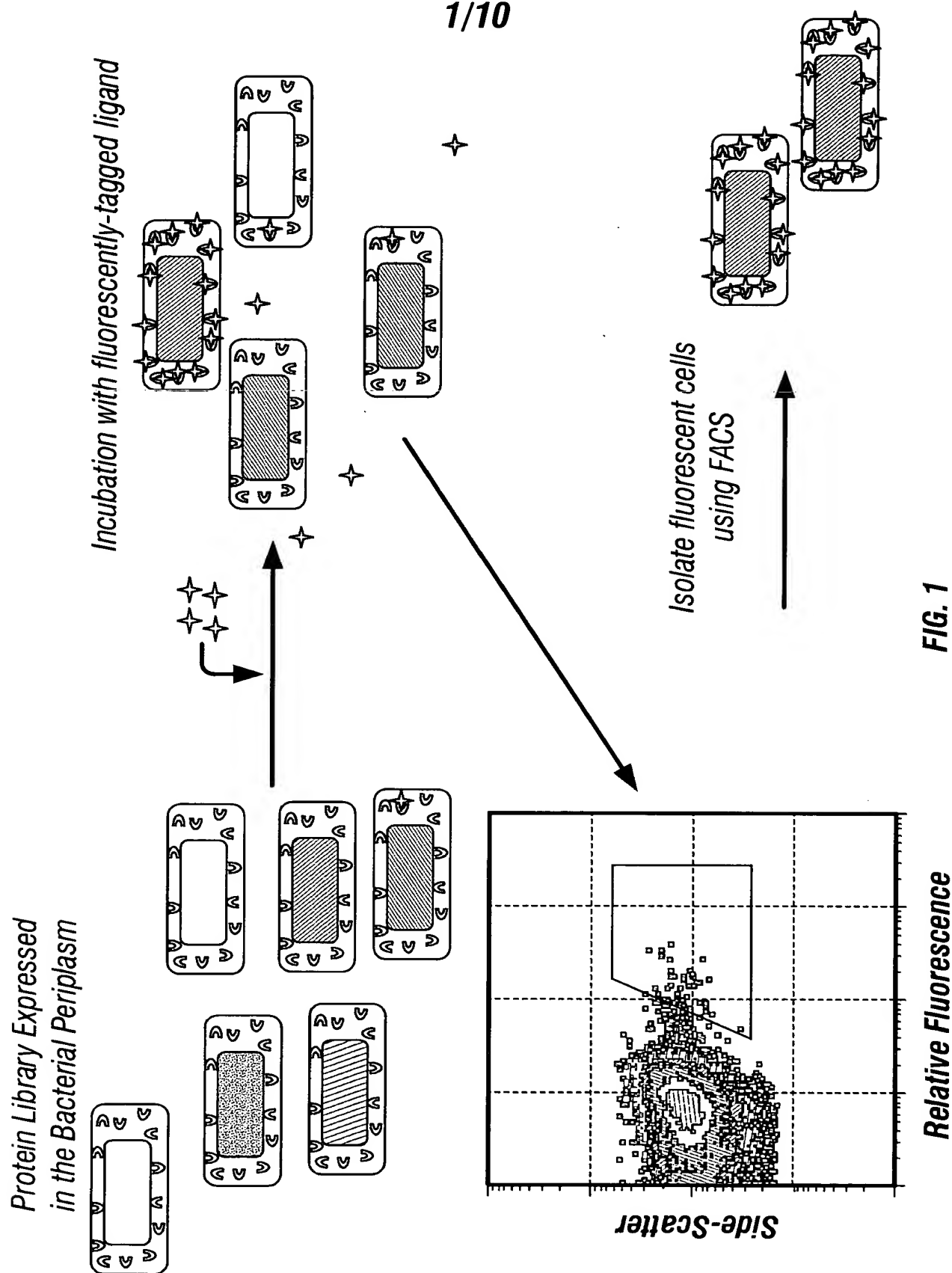
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1/10



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2/10

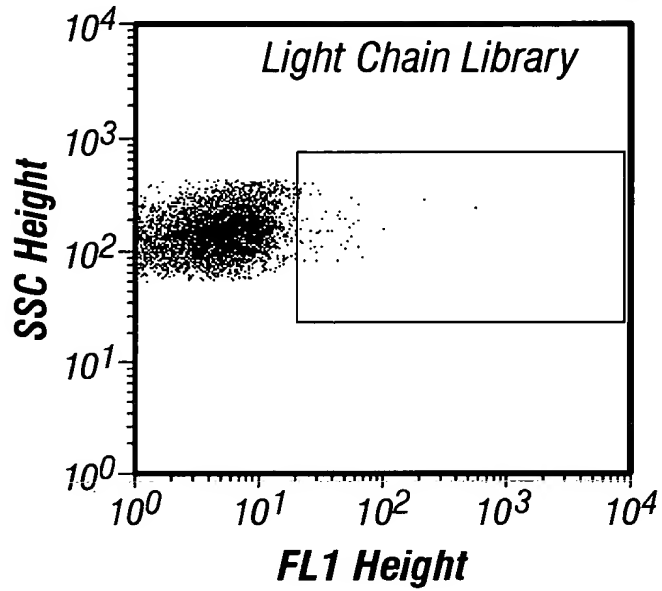


FIG. 2A

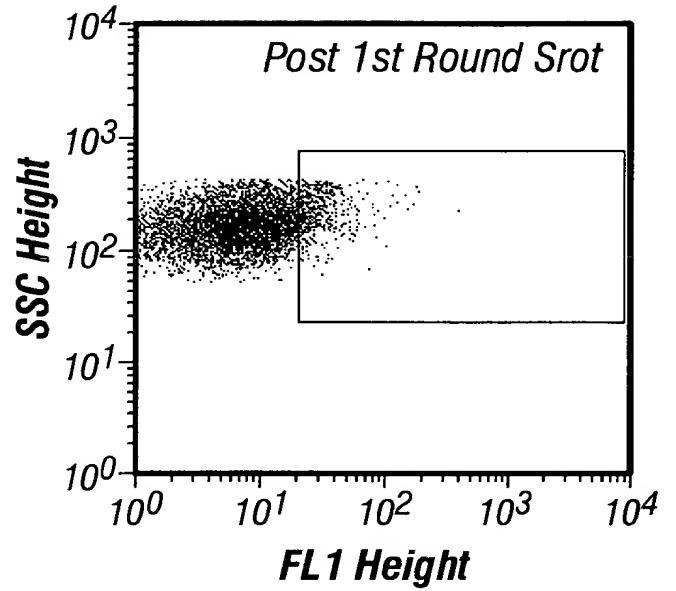


FIG. 2B

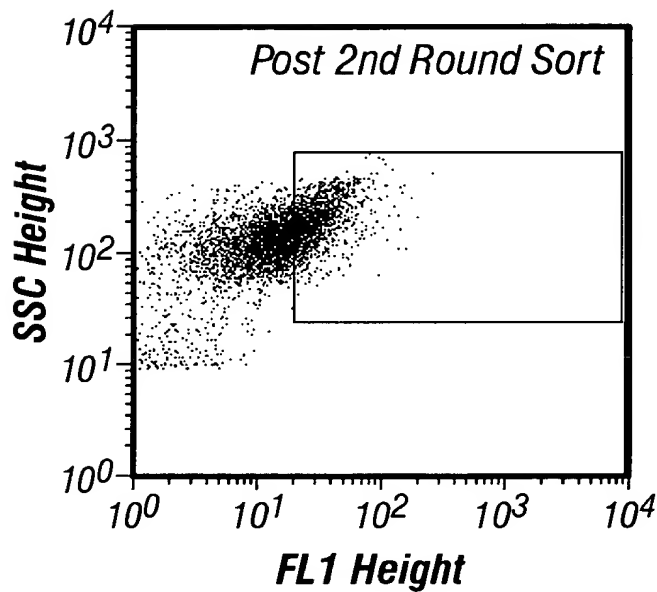
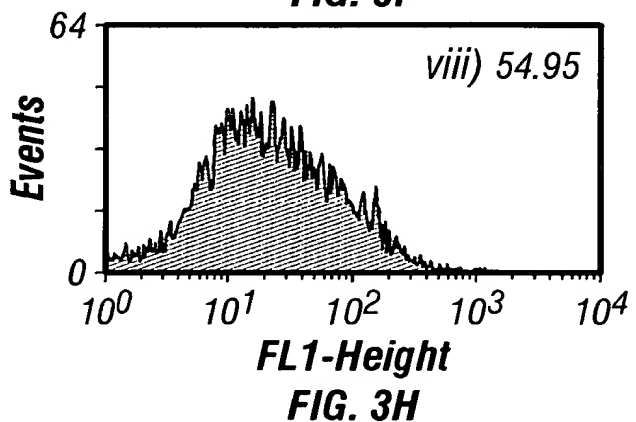
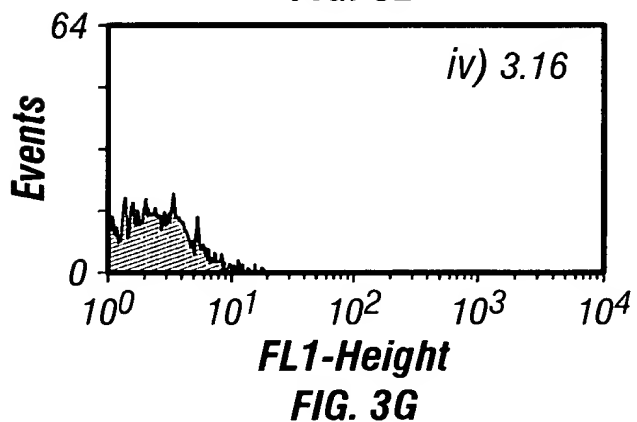
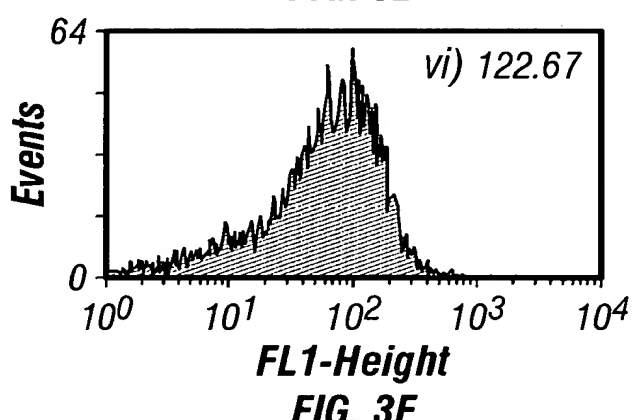
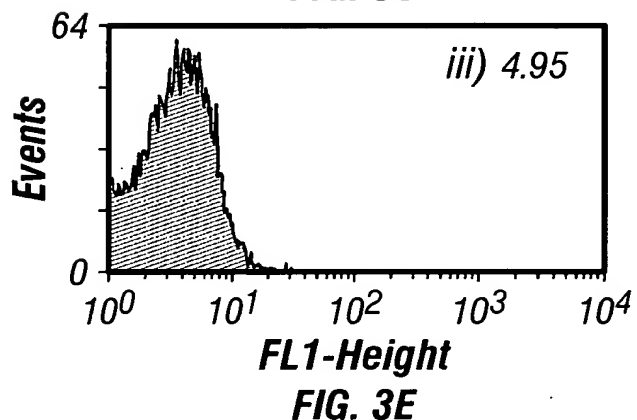
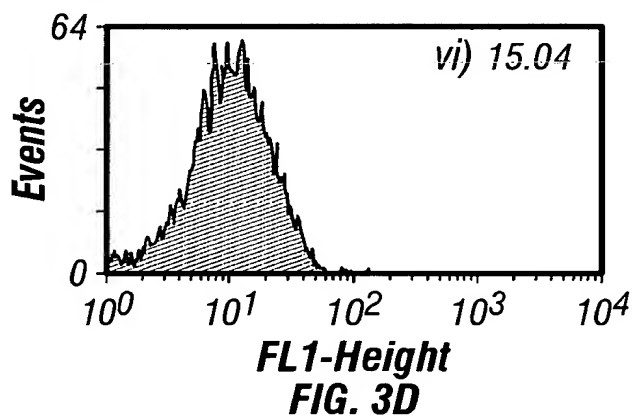
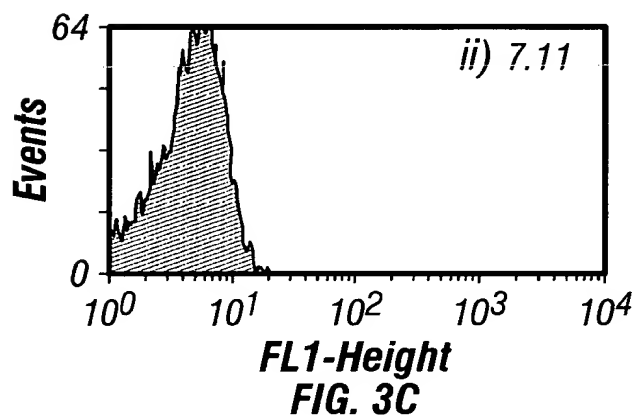
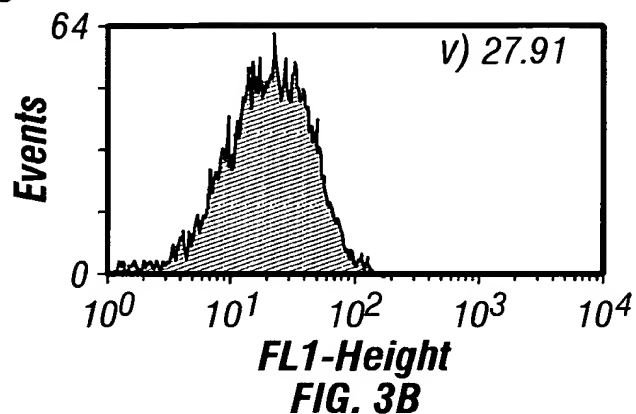
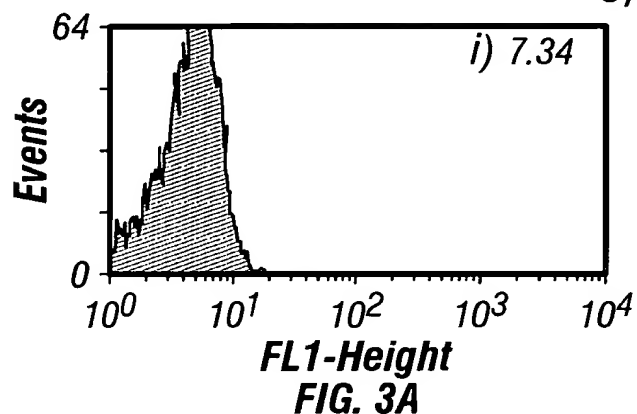


FIG. 2C

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3/10



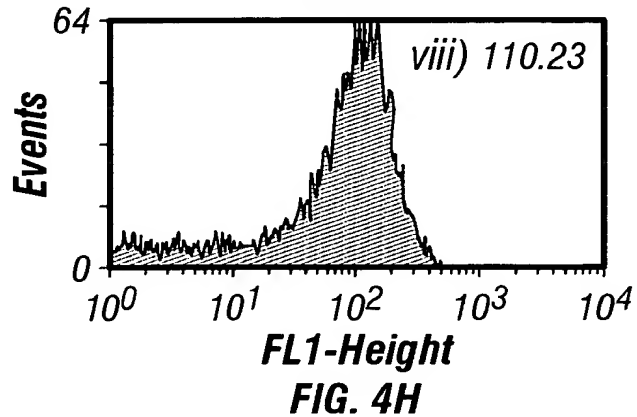
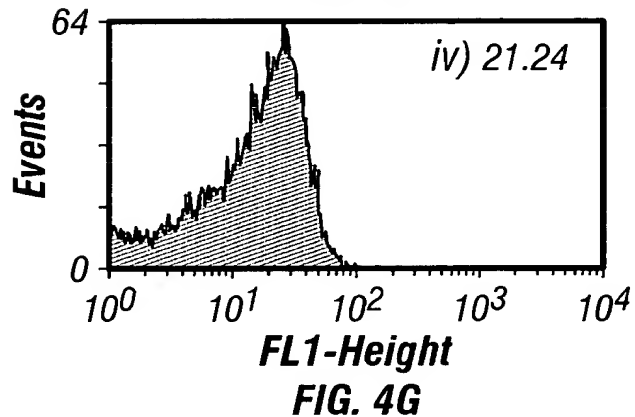
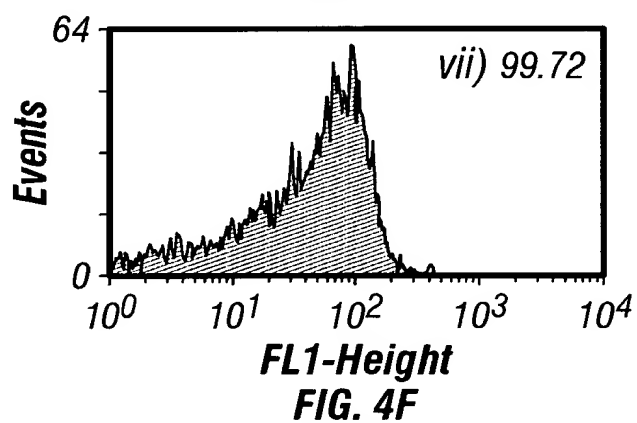
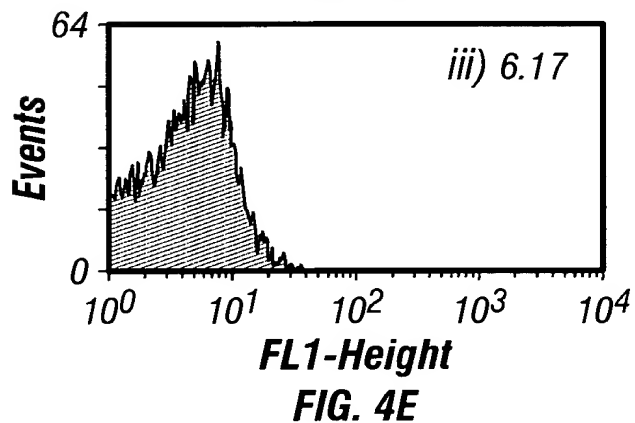
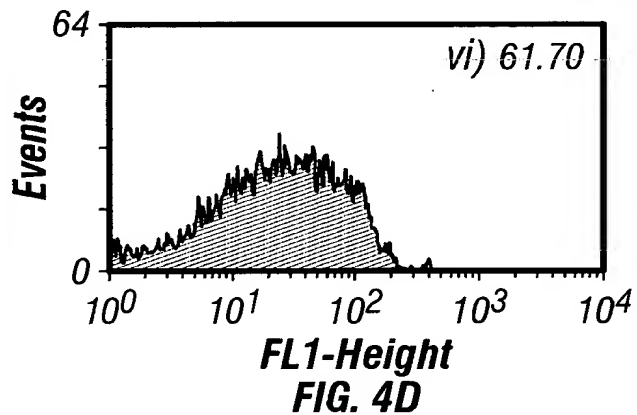
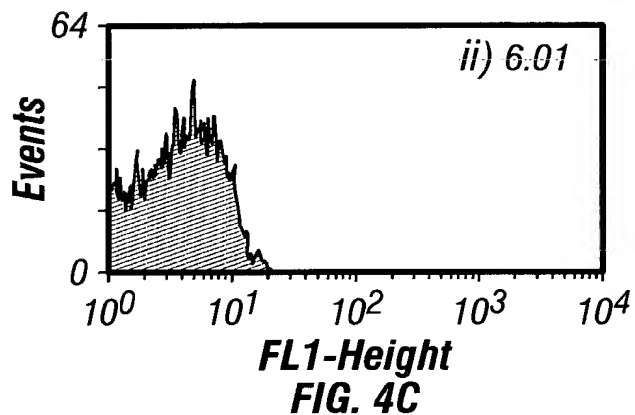
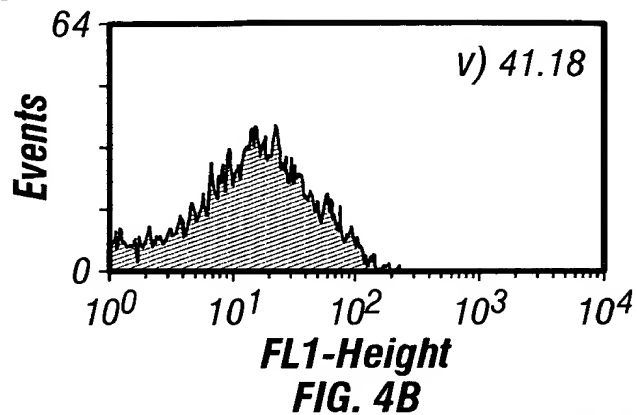
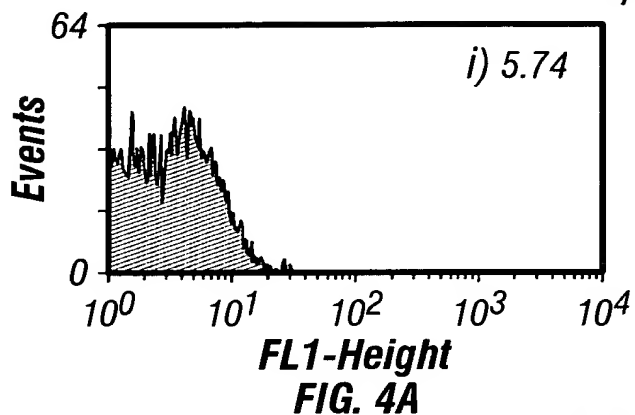
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Gang Chen et al.

4/10



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 Gang Chen et al.

5/10

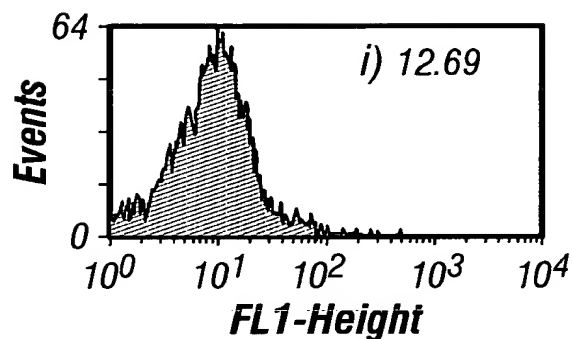


FIG. 5A

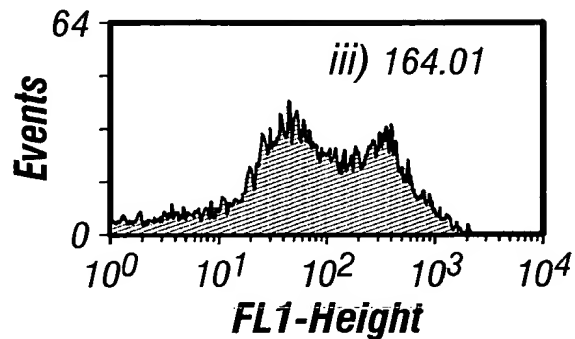


FIG. 5B

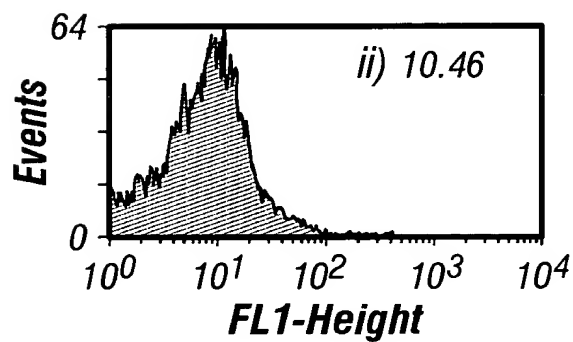


FIG. 5C

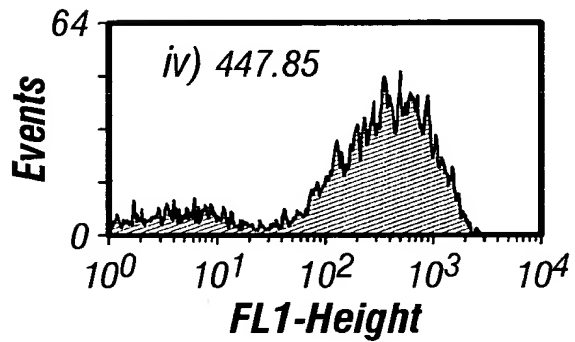


FIG. 5D

6/10

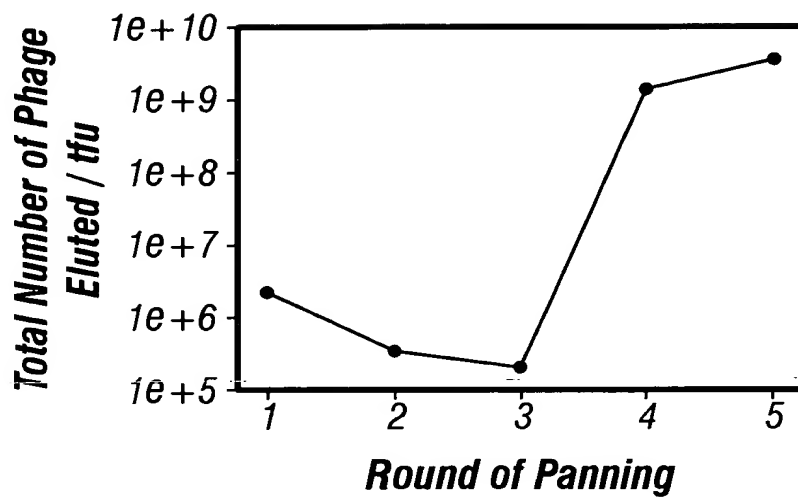


FIG. 6A

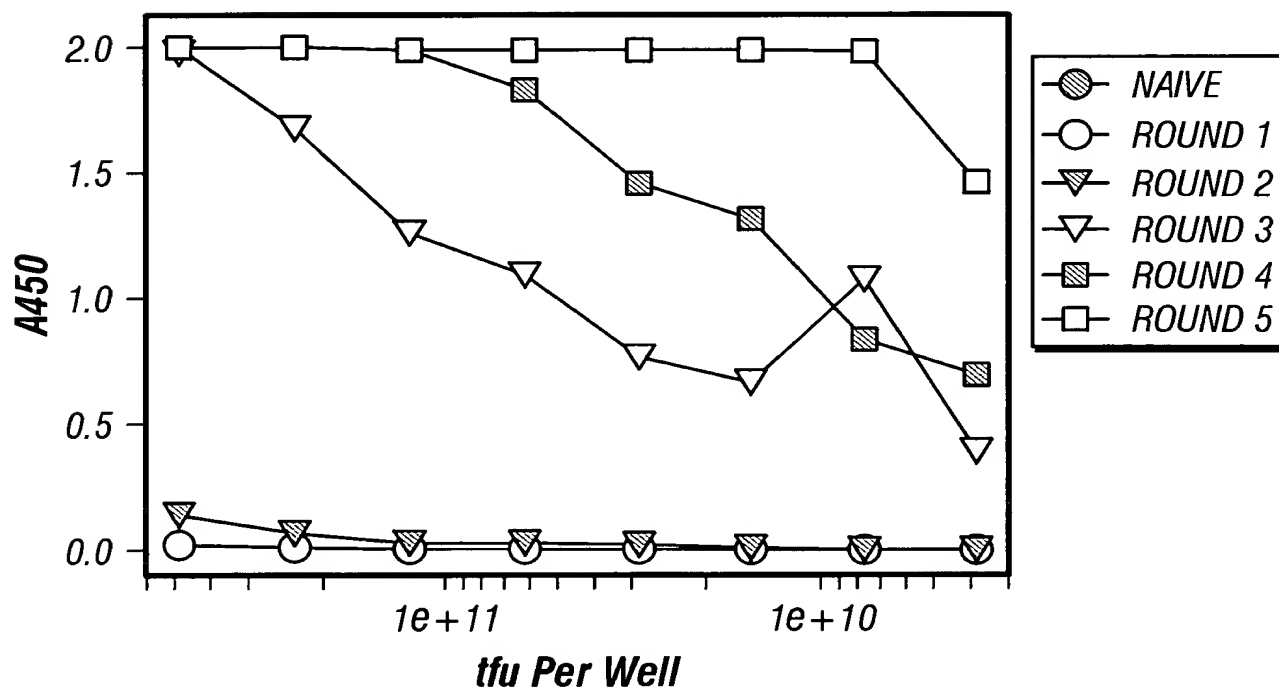
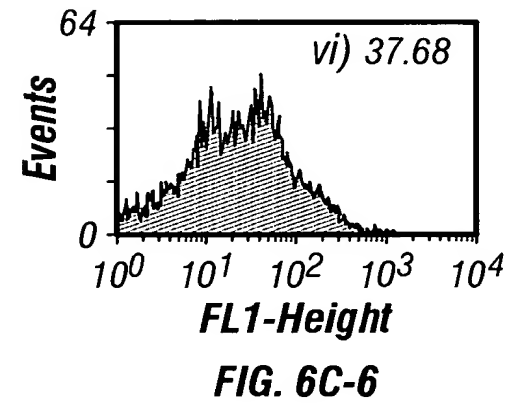
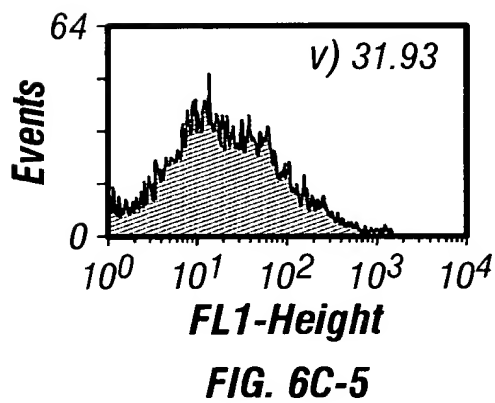
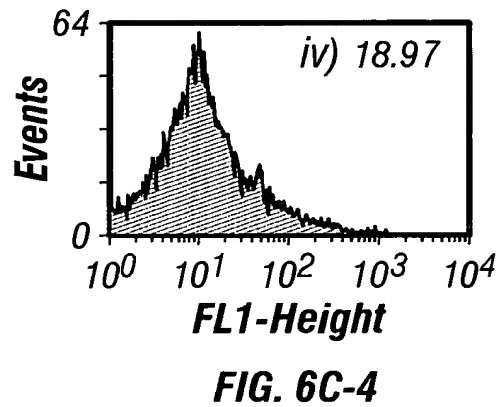
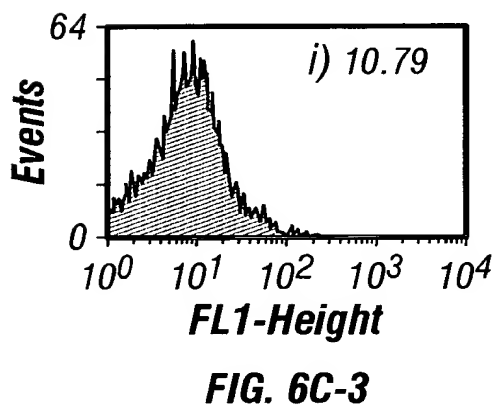
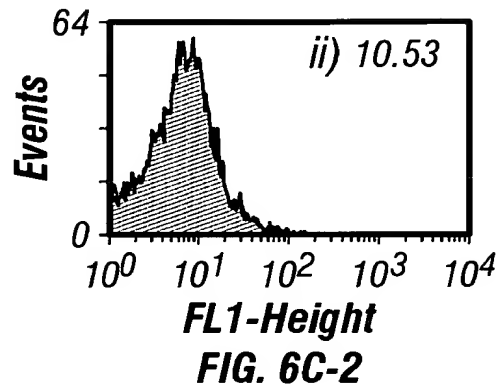
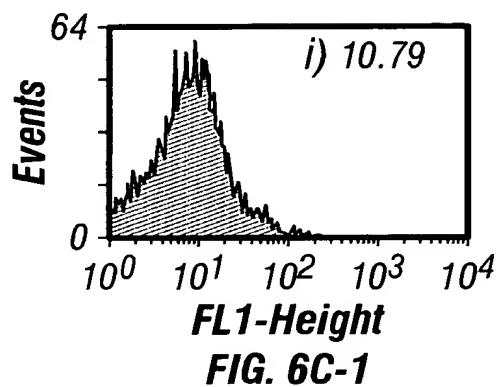


FIG. 6B

7/10



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"Isolation of Binding Proteins With High Affinity to Ligands"

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8/10

10

GlnValGlnLeuLeuGlnSerAlaAlaGluValLysLysProGlyGluSerLeuLys
 CAGGTGCAGCTGTTGCAGTCTGCAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAG
 G AG GG G GCT GTC T A G C GA
 ValGlu GlyGlyGlyLeuVal Gly Arg

20

30

CDR1

IleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArg
 ATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGC
 C GCA CC T C C GTGA AC GA A C
 Leu AlaAla PheThr SerAsp TyrMetSer Ile

40

52a

GlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAsp
 CAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGAT
 GCT A G G G TTCATAC TAG AG A GTAGTACC
 Ala ValSerTyr SerSerSerGly Thr

CDR2

70

ThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle
 ACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATC
 TATAC GCAGAC TG GA G GAT CAGG CG AG
 IleTyr AlaAsp ValLys ArgPhe Arg AsnAlaLys

80

82a b c

90

SerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSerAspThrAlaValTyrTyr
 AGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACGGCCGTGTATTAC
 A T ACTG T AAT A GA GA
 AsnSerLeu MetAsn Arg Glu

CDR3

110

CysAlaArgAlaSerProSerGlyPheAspTyrTrpGlyGlnGlyThrLeuValThr
 TGTGCAAGAGCTTCTCCTTCGGGGTTTGACTATTGGGGCCAAGGTACCCTGGTCACC
 ACGGG TT C
 ThrGlyPhePro
 A G AT
 ThrTyr

ValSerSer
 GTCTCGAGT

FIG. 7A

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 Gang Chen et al.

9/10

20
 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACC
 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThr

CDR1 31 a b
 ATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTACCAG
 IleSerCysSerGlySerSerSerAsnIleGlySerAsnTyrValTyrTrpTyrGln

40 CDR2
 CAGCTCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCA
 GlnLeuProGlyThrAlaProLysLeuLeuIleTyrArgAsnAsnGlnArgProSer

60 70
 GGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATC
 GlyValProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIle

80 CDR3
 AGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGC
 SerGlyLeuArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSer

95 a b 100
 CTGCGGGCTGTTGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
 LeuArgAlaValValPheGlyGlyGlyThrLysLeuThrValLeu

G G CC
 GlyGlyPro
 CTCG ---
 ProArg---

FIG. 7B

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10/10

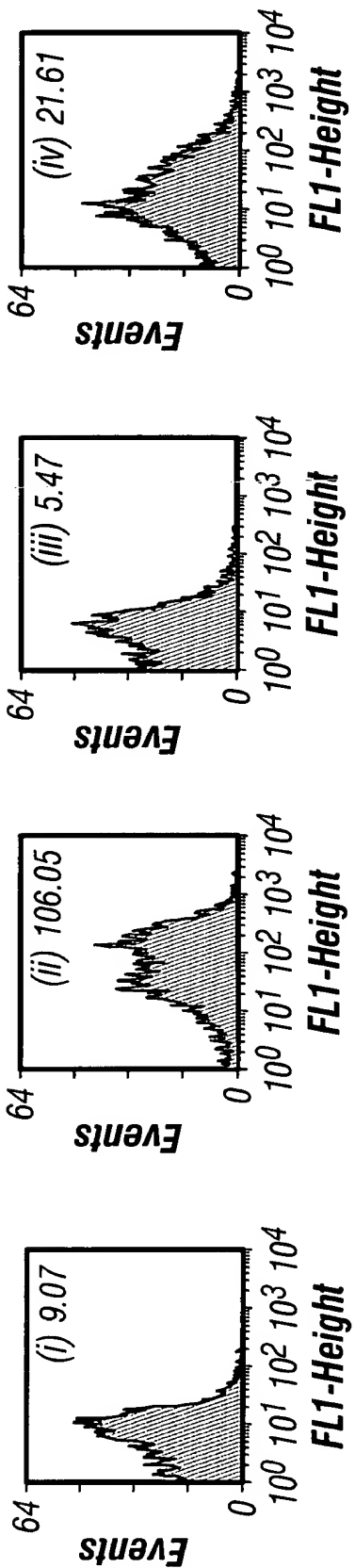


FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D

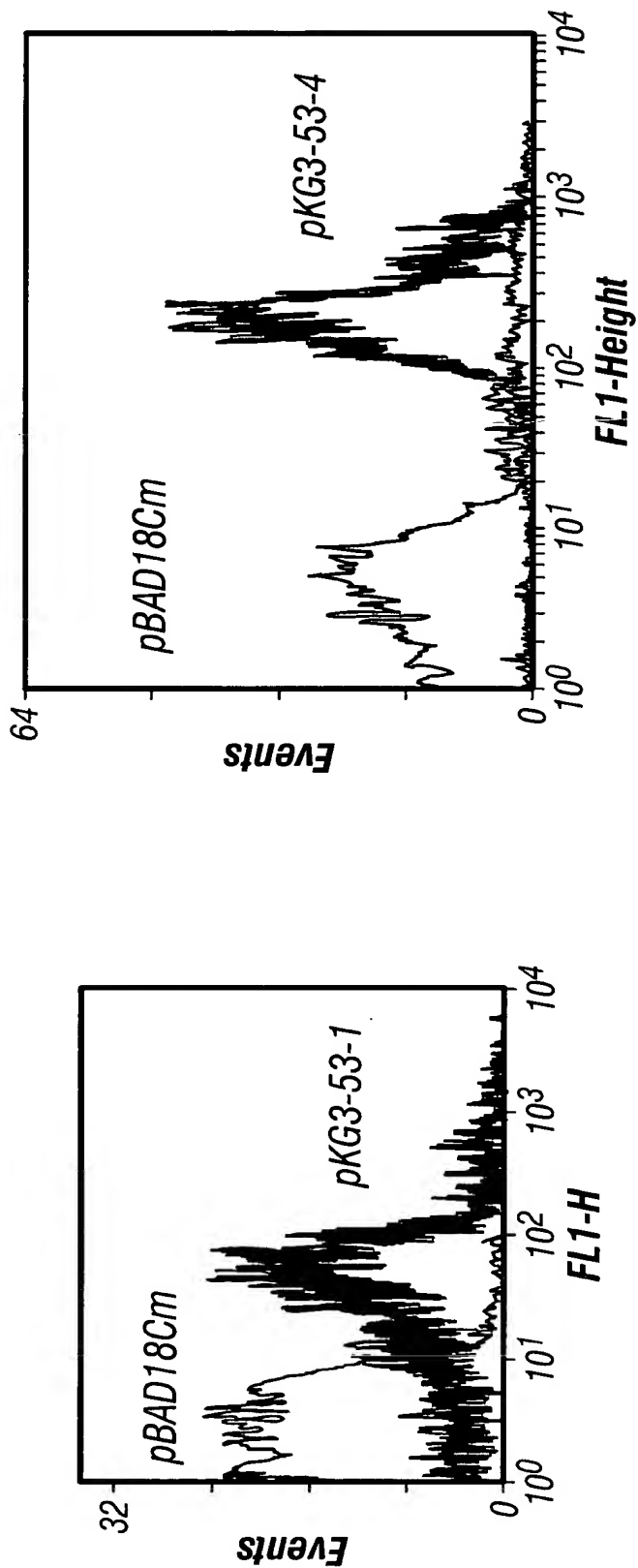


FIG. 9A

FIG. 9B